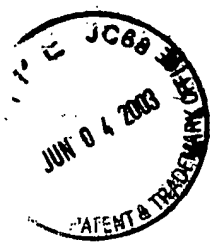


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GAATTCGGAG GAATTATTCA AAACATAAAC ACAATAAACA ATTTGAGTAG TTGCCGCACA 60
CACACACACA CACAGCCCGT GGATTATTAC ACTAAAAGCG ACACTCAATC CAAAAAATCA 120
GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA 171
Met His Trp Ile Lys Cys Leu Leu Thr Ala
1 5 10
TTC ATT TGC TTC ACA GTC ATC GTG CAG GTT CAC AGT TCC GGC AGC TTT 219
Phe Ile Cys Phe Thr Val Ile Val Gln Val His Ser Ser Gly Ser Phe
15 20 25
GAG TTG CGC CTG AAG TAC TTC AGC AAC GAT CAC GGG CGG GAC AAC GAG 267
Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asp His Gly Arg Asp Asn Glu
30 35 40
GGT CGC TGC TGC AGC GGG GAG TCG GAC GGA GCG ACG GGC AAG TGC CTG 315
Gly Arg Cys Cys Ser Gly Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu
45 50 55
GGC AGC TGC AAG ACG CGG TTT CGC GTC TGC CTA AAG CAC TAC CAG GCC 363
Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Gln Ala
60 65 70
ACC ATC GAC ACC ACC TCC CAG TGC ACC TAC GGG GAC GTG ATC ACG CCC 411
Thr Ile Asp Thr Thr Ser Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro
75 80 85 90
ATT CTC GGC GAG AAC TCG GTC AAT CTG ACC GAC GCC CAG CGC TTC CAG 459
Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asp Ala Gln Arg Phe Gln
95 100 105
AAC AAG GGC TTC ACG AAT CCC ATC CAG TTC CCC TTC TCG TTC TCA TGG 507
Asn Lys Gly Phe Thr Asn Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp
110 115 120

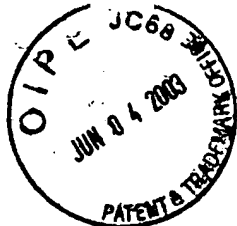
FIG. 10A



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CCG GGT ACC TTC TCG CTG ATC GTC GAG GCC TGG CAT GAT ACG AAC AAT Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asp Thr Asn Asn 125 130 135	555
AGC GGC AAT GCG CGA ACC AAC AAG CTC CTC ATC CAG CGA CTC TTG GTG Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Gln Arg Leu Leu Val 140 145 150	603
CAG CAG GTA CTG GAG GTG TCC TCC GAA TGG AAG ACG AAC AAG TCG GAA Gln Gln Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu 155 160 165 170	651
TCG CAG TAC ACG TCG CTG GAG TAC GAT TTC CGT GTC ACC TGC GAT CTC Ser Gln Tyr Thr Ser Leu Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu 175 180 185	699
AAC TAC TAC GGA TCC GGC TGT GCC AAG TTC TGC CGG CCC CGC GAC GAT Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp 190 195 200	747
TCA TTT GGA CAC TCG ACT TGC TCG GAG ACG GGC GAA ATT ATC TGT TTG Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu 205 210 215	795
ACC GGA TGG CAG GGC GAT TAC TGT CAC ATA CCC AAA TGC GCC AAA GGC Thr Gly Trp Gln Gly Asp Tyr Cys His Ile Pro Lys Cys Ala Lys Gly 220 225 230	843
TGT GAA CAT GGA CAT TGC GAC AAA CCC AAT CAA TGC GTT TGC CAA CTG Cys Glu His Gly His Cys Asp Lys Pro Asn Gln Cys Val Cys Gln Leu 235 240 245 250	891
GGC TGG AAG GGA GCC TTG TGC AAC GAG TGC GTT CTG GAA CCG AAC TGC Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys 255 260 265	939

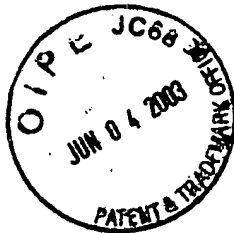
FIG. 10B



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ATC CAT GGC ACC TGC AAC AAA CCC TGG ACT TGC ATC TGC AAC GAG GGT Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly 270 275 280	987
TGG GGA GGC TTG TAC TGC AAC CAG GAT CTG AAC TAC TGC ACC AAC CAC Trp Gly Gly Leu Tyr Cys Asn Gln Asp Leu Asn Tyr Cys Thr Asn His 285 290 295	1035
AGA CCC TGC AAG AAT GGC GGA ACC TGC TTC AAC ACC GGC GAG GGA TTG Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu 300 305 310	1083
TAC ACA TGC AAA TGC GCT CCA GGA TAC AGT GGT GAT GAT TGC GAA AAT Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn 315 320 325 330	1131
GAG ATC TAC TCC TGC GAT GCC GAT GTC AAT CCC TGC CAG AAT GGT GGT Glu Ile Tyr Ser Cys Asp Ala Asp Val Asn Pro Cys Gln Asn Gly Gly 335 340 345	1179
ACC TGC ATC GAT GAG CCG CAC ACA AAA ACC GGC TAC AAG TGT CAT TGC Thr Cys Ile Asp Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys 350 355 360	1227
GCC AAC GGC TGG AGC GGA AAG ATG TGC GAG GAG AAA GTG CTC ACG TGT Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys 365 370 375	1275
TGC GAC AAA CCC TGT CAT CAG GGA ATC TGC CGC AAC GTT CGT CCT GGC Ser Asp Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly 380 385 390	1323
TTG GGA AGC AAG GGT CAG GGC TAC CAG TGC GAA TGT CCC ATT GGC TAC Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr 395 400 405 410	1371

FIG. 10C



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AGC GGA CCC AAC TGC GAT CTC CAG CTG GAC AAC TGC AGT CCG AAT CCA
Ser Gly Pro Asn Cys Asp Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro
415 420 425

TGC ATA AAC GGT GGA AGC TGT CAG CCG AGC GGA AAG TGT ATT TGC CCA 1467
Cys Ile Asn Gly Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro
430 435 440

GCG GGA TTT TCG GGA ACG AGA TGC GAG ACC AAC ATT GAC GAT TGT CTT 1515
Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu
445 450 455

GGC CAC CAG TGC GAG AAC GGA GGC ACC TGC ATA GAT ATG GTC AAC CAA 1563
Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asp Met Val Asn Gln
460 465 470

TAT CGC TGC CAA TGC GTT CCC GGT TTC CAT GGC ACC CAC TGT AGT AGC 1611
Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser
475 480 485 490

AAA GTT GAC TTG TGC CTC ATC AGA CCG TGT GCC AAT GGA GGA ACC TGC 1659
Lys Val Asp Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys
495 500 505

TTG AAT CTC AAC AAC GAT TAC CAG TGC ACC TGT CGT GCG GGA TTT ACT 1707
Leu Asn Leu Asn Asn Asp Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr
510 515 520

GGC AAG GAT TGC TCT GTG GAC ATC GAT GAG TGC AGC AGT GGA CCC TGT 1755
Gly Lys Asp Cys Ser Val Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys
525 530 535

CAT AAC GGC GGC ACT TGC ATG AAC CGC GTC AAT TCG TTC GAA TGC GTG 1803
His Asn Gly Gly Thr Cys Met Asn Arg Val Asn Ser Phe Glu Cys Val
540 545 550

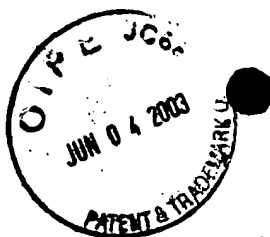
FIG. 10D



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TGT GCC AAT GGT TTC AGG GGC AAG CAG TGC GAT GAG GAG TCC TAC GAT Cys Ala Asn Gly Phe Arg Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp 555 560 565 570	1851
TCG GTG ACC TTC GAT GCC CAC CAA TAT GGA GCG ACC ACA CAA GCG AGA Ser Val Thr Phe Asp Ala His Gln Tyr Gly Ala Thr Thr Gln Ala Arg 575 580 585	1899
GCC GAT GGT TTG ACC AAT GCC CAG GTA GTC CTA ATT GCT GTT TTC TCC Ala Asp Gly Leu Thr Asn Ala Gln Val Val Leu Ile Ala Val Phe Ser 590 595 600	1947
GTT GCG ATG CCT TTG GTG GCG GTT ATT GCG GCG TGC GTG GTC TTC TGC Val Ala Met Pro Leu Val Ala Val Ile Ala Ala Cys Val Val Phe Cys 605 610 615	1995
ATG AAG CGC AAG CGT AAG CGT GCT CAG GAA AAG GAC GAC GCG GAG GCC Met Lys Arg Lys Arg Lys Arg Ala Gln Glu Lys Asp Asp Ala Glu Ala 620 625 630	2043
AGG AAG CAG AAC GAA CAG AAT GCG GTG GCC ACA ATG CAT CAC AAT GGC Arg Lys Gln Asn Glu Gln Asn Ala Val Ala Thr Met His His Asn Gly 635 640 645 650	2091
AGT GGG GTG GGT GTA GCT TTG GCT TCA GCC TCT CTG GGC GGC AAA ACT Ser Gly Val Gly Val Ala Leu Ala Ser Ala Ser Leu Gly Gly Lys Thr 655 660 665	2139
GGC AGC AAC AGC GGT CTC ACC TTC GAT GGC GGC AAC CCG AAT ATC ATC Gly Ser Asn Ser Gly Leu Thr Phe Asp Gly Gly Asn Pro Asn Ile Ile 670 675 680	2187
AAA AAC ACC TGG GAC AAG TCG GTC AAC AAC ATT TGT GCC TCA GCA GCA Lys Asn Thr Trp Asp Lys Ser Val Asn Asn Ile Cys Ala Ser Ala Ala 685 690 695	2235

FIG. 10E



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GCA GCG GCG GCG GCG GCA GCA GCG GCG GAC GAG TGT CTC ATG TAC GGC Ala Ala Ala Ala Ala Ala Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly 700 705 710	2283
GGA TAT GTG GCC TCG GTG GCG GAT AAC AAC AAT GCC AAC TCA GAC TTT Gly Tyr Val Ala Ser Val Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe 715 720 725 730	2331
TGT GTG GCT CCG CTA CAA AGA GCC AAG TCG CAA AAG CAA CTC AAC ACC Cys Val Ala Pro Leu Gln Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr 735 740 745	2379
GAT CCC ACG CTC ATG CAC CGC GGT TCG CCG GCA GGC AGC TCA GCC AAG Asp Pro Thr Leu Met His Arg Gly Ser Pro Ala Gly Ser Ser Ala Lys 750 755 760	2427
GGA GCG TCT GGC GGA GGA CCG GGA GCG GCG GAG GGC AAG AGG ATC TCT Gly Ala Ser Gly Gly Gly Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser 765 770 775	2475
GTT TTA GGC GAG GGT TCC TAC TGT AGC CAG CGT TGG CCC TCG TTG GCG Val Leu Gly Glu Gly Ser Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala 780 785 790	2523
GCG GCG GGA GTG GCC GGA GCC TGT TCA TCC CAG CTA ATG GCT GCA GCT Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Gln Leu Met Ala Ala Ala 795 800 805 810	2571
TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG CGA TCC GTG Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val 815 820 825	2619
GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT Val Cys Gly Thr Pro His Met 830	2670
AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGGT GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTGTGTG ATTGAAGCAG TTTAGTCGTC ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC	2730 2790 2850 2892

FIG. 10F



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10	20	30	40	50	60
GAATTCCCT	CCCCCTTT	TCCATGCAGC	TGATCTAAAA	GGGAATAAAA	GGCTGCGCAT
70	80	90	100	110	120
AATCATAATA	ATAAAAGAAG	GGGAGCGCGA	GAGAAGGAAA	GAAAGCCGGG	AGGTGGAAGA
130	140	150	160	170	180
GGAGGGGGAG	CGTCTCAAAG	AAGCGATCAG	AATAATAAAA	GGAGGCCGGG	CTCTTTGCCT
190	200	210	220	230	240
TCTGGAAGGG	GCCGCTCTTG	AAAGGGCTTT	TGAAAAGTGG	TGTTGTTTTT	CAGTCGTGCA
250	260	270	280	290	300
TGCTCCAATC	GGCGGAGTAT	ATTAGAGCCG	GGACGCGGCC	GCAGGGGCAG	CGGCGACGGC
310	320	330	340	350	360
AGCACCGGCG	GCAGCACCAG	CGCGAACAGC	AGCGGCGGCG	TCCCAGAGTC	CCGCGGCGGC
370	380	390	400	410	420
GCGCGCAGCG	ATGCGTTCCC	CACGGACACG	CGGCCGGTCC	GGGCGCCCCC	TAAGCCTCCT
	M R S	P R T R	G R S	G R P	L S L L>
430	440	450	460	470	480
GCTCGCCCTG	CTCTGTGCCC	TGCGAGCCAA	GGTGTGTGGG	GCCTCGGGTC	AGTTCGAGTT
L A L	L C A	L R A K	V C G	A S G	Q F E L>
490	500	510	520	530	540
GGAGATCCTG	TCCATGCAGA	ACGTGAACGG	GGAGCTGCAG	AACGGGAACT	GCTGCGGCGG
E I L	S M Q	N V N G	E L Q	N G N	C C G G>
550	560	570	580	590	600
CGCCCGGAAC	CCGGGAGACC	GCAAGTGCAC	CCGCGACGAG	TGTGACACAT	ACTTCAAAGT
A R N	P G D	R K C T	R D E	C D T	Y F K V>
610	620	630	640	650	660
GTGCCTCAAG	GAGTATCAGT	CCCGCGTCAC	GGCCGGGGGG	CCCTGCAGCT	TCGGCTCAGG
C L K	E Y Q	S R V T	A G G	P C S	F G S G>
670	680	690	700	710	720
GTCCACGCCT	GTCATCGGGG	GCAACACCTT	CAACCTCAAG	GCCAGCCGCG	GCAACGACCC
S T P	V I G	G N T F	N L K	A S P	G N D P>
730	740	750	760	770	780
GAACCGCATC	GTGCTGCCTT	TCAGTTTCGC	CTGGCCGAGG	TCCTATACGT	TGCTTGTGGA
N R I	V L P	F S F A	W P R	S Y T	L L V E>
790	800	810	820	830	840
GGCGTGGGAT	TCCAGTAATG	ACACCGTTCA	ACCTGACAGT	ATTATTGAAA	AGGCTTCTCA
A W D	S S N	D T V Q	P D S	I I E	K A S H>
850	860	870	880	890	900
CTCGGGCATG	ATCAACCCCA	GCCGGCAGTG	GCAGACGCTG	AAGCAGAACA	CGGGCGTTGC
S G M	I N P	S R Q W	Q T L	K Q N	T G V A>

FIG. 11A



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          910          920          930          940          950          960
CCACTTTGAG TATCAGATCC GCGTGACCTG TGATGACTAC TACTATGGCT TTGGCTGTAA
  H F E Y Q I R V T C D D Y Y Y G F G C N>
          970          980          990          1000          1010          1020
TAAGTTCTGC CGCCCCAGAG ATGACTTCTT TGGACACTAT GCCTGTGACC AGAATGGCAA
  K F C R P R D D F F G H Y A C D Q N G N>
          1030          1040          1050          1060          1070          1080
CAAACTTGC ATGGAAGGCT GGATGGGCCC CGAATGTAAC AGAGCTATTT GCCGACAAGG
  K T C M E G W M G P E C N R A I C R Q G>
          1090          1100          1110          1120          1130          1140
CTGCAGTCTT AAGCATGGGT CTTGCAAACT CCCAGGTGAC TGCAGGTGCC AGTACGGCTG
  C S P K H G S C K L P G D C R C Q Y G W>
          1150          1160          1170          1180          1190          1200
GCAAGGCCTG TACTGTGATA AGTGCATCCC ACACCCGGGA TGGCTCCACG GCATCTGTAA
  Q G L Y C D K C I P H P G C V H G I C N>
          1210          1220          1230          1240          1250          1260
TGAGCCCTGG CAGTGCCTCT GTGAGACCAA CTGGGGCGGC CAGCTCTGTG ACAAAGATCT
  E P W Q C L C E T N W G G Q L C D K D L>
          1270          1280          1290          1300          1310          1320
CAATTACTGT GGGACTCATC AGCCGTGTCT CAACGGGGGA ACTTGTAGCA ACACAGGCCC
  N Y C G T H Q P C L N G G T C S N T G P>
          1330          1340          1350          1360          1370          1380
TGACAAATAT CAGTGTTCCT GCCCTGAGGG GTATTGAGGA CCCAACTGTG AAATTGCTGA
  D K Y Q C S C P E G Y S G P N C E I A E>
          1390          1400          1410          1420          1430          1440
GCACGCCTGC CTCTCTGATC CCTGTCACAA CAGAGGCAGC TGTAAGGAGA CCTCCCTGGG
  H A C L S D P C H N R G S C K E T S L G>
          1450          1460          1470          1480          1490          1500
CTTTGAGTGT GAGTGTTCCT CAGGCTGGAC CGGCCCCACA TGCTCTACAA ACATTGATGA
  F E C E C S P G W T G P T C S T N I D D>
          1510          1520          1530          1540          1550          1560
CTGTTCTCCT AATAACTGTT CCCACGGGGG CACCTGCCAG GACCTGGTTA ACGGATTTAA
  C S P N N C S H G G T C Q D L V N G F K>
          1570          1580          1590          1600          1610          1620
GTGTGTGTGC CCCCCACAGT GGAATGGGAA AACGTGCCAG TTAGATGCAA ATGAATGTGA
  C V C P P Q W T G K T C Q L D A N E C E>
          1630          1640          1650          1660          1670          1680
GGCCAAACCT TGTGTAAACG CCAAATCTG TAAGAATCTC ATTGCCAGCT ACTACTGCCA
  A K P C V N A K S C K N L I A S Y Y C D>

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FIG. 11B



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1690	1700	1710	1720	1730	1740
CTGTCTTCCC	GGCTGGATGG	GTCAGAATTG	TGACATAAAT	ATTAATGACT	GCCTTGGCCA
C L P	G W M	G Q N C	D I N	I N D	C L G Q>
1750	1760	1770	1780	1790	1800
GTGTCAGAAT	GACGCCTCCT	GTCGGGATTT	GGTTAATGGT	TATCGCTGTA	TCTGTCCACC
C Q N	D A S	C R D L	V N G	Y R C	I C P P>
1810	1820	1830	1840	1850	1860
TGGCTATGCA	GGCGATCACT	GTGAGAGAGA	CATCGATGAA	TGTGCCAGCA	ACCCCTGTTT
G Y A	G D H	C E R D	I D E	C A S	N P C L>
1870	1880	1890	1900	1910	1920
GAATGGGGGT	CACTGTCAGA	ATGAAATCAA	CAGATTCCAG	TGTCTGTGTC	CCACTGGTTT
N G G	H C Q	N E I N	R F Q	C L C	P T G F>
1930	1940	1950	1960	1970	1980
CTCTGGAAC	CTCTGTCAGC	TGGACATCGA	TTATTGTGAG	CCTAATCCCT	GCCAGAACGG
S G N	L C Q	L D I D	Y C E	P N P	C Q N G>
1990	2000	2010	2020	2030	2040
TGCCCCAGTG	TACAACCGTG	CCAGTGACTA	TTTCTGCAAG	TGCCCCGAGG	ACTATGAGGG
A Q C	Y N R	A S D Y	F C K	C P E	D Y E G>
2050	2060	2070	2080	2090	2100
CAAGAACTGC	TCACACCTGA	AAGACCACTG	CCGCACGACC	CCCTGTGAAG	TGATTGACAG
K N C	S H L	K D H C	R T T	P C E	V I D S>
2110	2120	2130	2140	2150	2160
CTGCACAGTG	GCCATGGCTT	CCAACGACAC	ACCTGAAGGG	GTGCGGTATA	TTTCCTCCAA
C T V	A M A	S N D T	P E G	V R Y	I S S N>
2170	2180	2190	2200	2210	2220
CGTCTGTGGT	CCTCACGGGA	AGTGCAAGAG	TCAGTCGGGA	GGCAAATTCA	CCTGTGACTG
V C G	P H G	K C K S	Q S G	G K F	T C D C>
2230	2240	2250	2260	2270	2280
TAACAAAGGC	TTCACGGGAA	CATACTGCCA	TGAAAATATT	AATGACTGTG	AGAGCAACCC
N K G	F T G	T Y C H	E N I	N D C	E S N P>
2290	2300	2310	2320	2330	2340
TTGTAGAAAC	GGTGGCACTT	GCATCGATGG	TGTCAACTCC	TACAAGTGCA	TCTGTAGTGA
C R N	G G T	C I D G	V N S	Y K C	I C S D>
2350	2360	2370	2380	2390	2400
CGGCTGGGAG	GGGGCCTACT	GTGAAACCAA	TATTAATGAC	TGCAGCCAGA	ACCCCTGCCA
G W E	G A Y	C E T N	I N D	C S Q	N P C H>
2410	2420	2430	2440	2450	2460
CAATGGGGGC	ACGTGTCGCG	ACCTGGTCAA	TGACTTCTAC	TGTGACTGTA	AAAATGGGTG
N G G	T C R	D L V N	D F Y	C D C	K N G W>

FIG. 11C



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2470	2480	2490	2500	2510	2520
GAAAGGAAAG	ACCTGCCACT	CACGTGACAG	TCAGTGTGAT	GAGGCCACGT	GCAACAACGG
K G K	T C H	S R D S	Q C D	E A T	C N N G>
2530	2540	2550	2560	2570	2580
TGGCACCTGC	TATGATGAGG	GGGATGCTTT	TAAGTGCATG	TGTCCTGGCG	GCTGGGAAGG
G T C	Y D E	G D A F	K C M	C P G	G W E G>
2590	2600	2610	2620	2630	2640
AACAACCTGT	AACATAGCCC	GAAACAGTAG	CTGCCTGCCC	AACCCCTGCC	ATAATGGGGG
T T C	N I A	R N S S	C L P	N P C	H N G G>
2650	2660	2670	2680	2690	2700
CACATGTGTG	GTCAACGGCG	AGTCCTTTAC	GTGCGTCTGC	AAGGAAGGCT	GGGAGGGGGC
T C V	V N G	E S F T	C V C	K E G	W E G P>
2710	2720	2730	2740	2750	2760
CATCTGTGCT	CAGAATACCA	ATGACTGCAG	CCCTCATCCC	TGTTACAACA	GCGGCACCTG
I C A	Q N T	N D C S	P H P	C Y N	S G T C>
2770	2780	2790	2800	2810	2820
TGTGGATGGA	GACAACTGGT	ACCGGTGCGA	ATGTGCCCCG	GGTTTTGCTG	GGCCCCACTG
V D G	D N W	Y R C E	C A P	G F A	G P D C>
2830	2840	2850	2860	2870	2880
CAGAATAAAC	ATCAATGAAT	GCCAGTCTTC	ACCTTGTGCC	TTTGGAGCGA	CCTGTGTGGA
R I N	I N E	C Q S S	P C A	F G A	T C V D>
2890	2900	2910	2920	2930	2940
TGAGATCAAT	GGCTACCGGT	GTGTCTGCCC	TCCAGGGCAC	AGTGGTGCCA	AGTGCCAGGA
E I N	G Y R	C V C P	P G H	S G A	K C Q E>
2950	2960	2970	2980	2990	3000
AGTTTCAGGG	AGACCTTGCA	TCACCATGGG	GAGTGTGATA	CCAGATGGGG	CCAAATGGGA
V S G	R P C	I T M G	S V I	P D G	A K W D>
3010	3020	3030	3040	3050	3060
TGATGACTGT	AATACCTGCC	AGTGCCTGAA	TGGACGGATC	GCCTGCTCAA	AGGTCTGGTG
D D C	N T C	Q C L N	G R I	A C S	K V W C>
3070	3080	3090	3100	3110	3120
TGGCCCTCGA	CCTTGCTGCT	TCCACAAAGG	GCACAGCGAG	TGCCCCAGCG	GGCAGAGCTG
G P R	P C L	L H K G	H S E	C P S	G Q S C>
3130	3140	3150	3160	3170	3180
CATCCCCATC	CTGGACGACC	AGTGCCTCGT	CCACCCCTGC	ACTGGTGTGG	GCGAGTGTG
I P I	L D D	Q C F V	H P C	T G V	G E C R>
3190	3200	3210	3220	3230	3240
GTCTTCCAGT	CTCCAGCCGG	TGAAGACAAA	GTGCACCTCT	GACTCCTATT	ACCAGGATAA
S S S	L Q P	V K T K	C T S	D S Y	Y Q D N>
3250	3260	3270	3280	3290	3300
CTGTGCGAAC	ATCACATTTA	CCTTTAACAA	GGAGATGATG	TCACCAGGTC	TTACTACGGA
C A N	I T F	T F N K	E M M	S P G	L T T E>

FIG. 11D



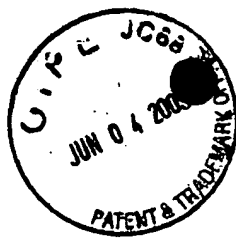
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3310      3320      3330      3340      3350      3360
GCACATTTGC AGTGAATTGA GGAATTTGAA TATTTTGAAG AATGTTTCCG CTGAATATTC
  H I C   S E L   R N L N   I L K   N V S   A E Y S>
3370      3380      3390      3400      3410      3420
AATCTACATC GCTTGCGAGC CTTCCCCTTC AGCGAACAAT GAAATACATG TGGCCATTTC
  I Y I   A C E   P S P S   A N N   E I H   V A I S>
3430      3440      3450      3460      3470      3480
TGCTGAAGAT ATACGGGATG ATGGGAACCC GATCAAGGAA ATCACTGACA AAATAATCGA
  A E D   I R D   D G N P   I K E   I T D   K I I D>
3490      3500      3510      3520      3530      3540
TCTTGTTACT AAACGTGATG GAAACAGCTC GCTGATTGCT GCCGTTGAAG AAGTAAGAGT
  L V T   K R D   G N S S   L I A   A V E   E V R V>
3550      3560      3570      3580      3590      3600
TCAGAGGCGG CCTCTGAAGA ACAGAACAGA TTTCCTTGTT CCCTTGCTGA GCTCTGTCTT
  Q R R   P L K   N R T D   F L V   P L L   S S V L>
3610      3620      3630      3640      3650      3660
AACTGTGGCT TGGATCTGTT GCTTGGTGAC GGCCTTCTAC TGGTGCCTGC GGAAGCGGGC
  T V A   W I C   C L V T   A F Y   W C L   R K R R>
3670      3680      3690      3700      3710      3720
GAAGCCGGGC AGCCACACAC ACTCAGCCTC TGAGGACAAC ACCACCAACA ACGTGCGGGA
  K P G   S H T   H S A S   E D N   T T N   N V R E>
3730      3740      3750      3760      3770      3780
GCAGCTGAAC CAGATCAAAA ACCCCATTGA GAAACATGGG GCCAACACGG TCCCCATCA
  Q L N   Q I K   N P I E   K H G   A N T   V P I K>
3790      3800      3810      3820      3830      3840
GGATTACGAG AACAAGAACT CCAAAATGTC TAAAATAAGG ACACACAATT CTGAAGTAGA
  D Y E   N K N   S K M S   K I R   T H N   S E V E>
3850      3860      3870      3880      3890      3900
AGAGGACGAC ATGGACAAAC ACCAGCAGAA AGCCCGGTTT GCCAAGCAGC CGGCGTACAC
  E D D   M D K   H Q Q K   A R F   A K Q   P A Y T>
3910      3920      3930      3940      3950      3960
GCTGGTAGAC AGAGAAGAGA AGCCCCCAA CGGCACGCCG ACAAACACC CAACTGGAC
  L V D   R E E   K P P N   G T P   T K H   P N W T>
3970      3980      3990      4000      4010      4020
AAACAAACAG GACAACAGAG ACTTGAAAG TGCCCAGAGC TTAAACCGAA TGGAGTACAT
  N K Q   D N R   D L E S   A Q S   L N R   M E Y I>
4030      4040      4050      4060      4070      4080
CGTATAGCAG ACCGCGGGCA CTGCCGCCGC TAGGTAGAGT CTGAGGGCTT GTAGTTCTTT
V >

```

FIG. 11E



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4090	4100	4110	4120	4130	4140
AAACTGTCGT	GTCATACTCG	AGTCTGAGGC	CGTTGCTGAC	TTAGAATCCC	TGTGTTAATT
4150	4160	4170	4180	4190	4200
TAGTTTGACA	AGCTGGCTTA	CACTGGCAAT	GGTAGTTCTG	TGGTTGGCTG	GGAAATCGAG
4210	4220	4230	4240	4250	4260
TGGCGCATCT	CACAGCTATG	CAAAAAGCTA	GTCAACAGTA	CCCCTGGTTG	TGTGTCCCCT
4270	4280	4290	4300	4310	4320
TGCAGCCGAC	ACGGTCTCGG	ATCAGGCTCC	CAGGAGCTGC	CCAGCCCCCT	GGTACTTTGA
4330	4340	4350	4360	4370	4380
GCTCCCACTT	CTGCCAGATG	TCTAATGGTG	ATGCAGTCTT	AGATCATAGT	TTTATTTATA
4390	4400	4410	4420	4430	4440
TTTATTGACT	CTTGAGTTGT	TTTTGTATAT	TGGTTTTATG	ATGACGTACA	AGTAGTTCCTG
4450	4460	4470	4480	4490	4500
TATTTGAAAG	TGCCTTTGCA	GCTCAGAACC	ACAGCAACGA	TCACAAATGA	CTTTATTATT
4510	4520	4530	4540	4550	4560
TATTTTTTTT	AATTGTATTT	TTGTTGTTGG	GGGAGGGGAG	ACTTTGATGT	CAGCAGTTGC
4570	4580	4590	4600	4610	4620
TGGTAAATG	AAGAATTTAA	AGAAAAAATG	TCCAAAAGTA	GAACTTTGTA	TAGTTATGTA
4630	4640	4650	4660	4670	4680
AATAATTCTT	TTTTATTAAT	CACTGTGTAT	ATTTGATTTA	TTAACTTAAT	AATCAAGAGC
4690	4700	4710	4720	4730	4740
CTTAAACAT	CATTCCTTTT	TATTTATATG	TATGTGTTTA	GAATTGAAGG	TTTTTGATAG
4750	4760	4770	4780	4790	4800
CATTGTAAGC	GTATGGCTTT	ATTTTTTTGA	ACTCTTCTCA	TTACTTGTTG	CCTATAAGCC
4810	4820	4830	4840	4850	4860
AAAAAGGAAA	GGGTGTTTTG	AAAATAGTTT	ATTTTAAAC	AATAGGATGG	GCTACACGTA
4870	4880	4890	4900	4910	4920
CATAGGTAA	TAATAGCACC	GTAAGGTTA	TGATGATGAA	AATAACTGGA	AACTTGAAAG
4930	4940	4950	4960	4970	4980
CTTGTGGTAA	TGGCAGATAA	AGATGGTTCA	CCTGGGAAAT	TAAAACTTGA	ATGGTTGTAC
4990	5000	5010	5020	5030	5040
AGAAAAGCAC	AGAGTGGAAT	GCACATCAAT	GACAGTAAGG	GAGTTAGTTC	TAGGAACAGC
5050	5060	5070	5080	5090	5100
TCCTGAACAG	TAAGATTCCC	GCAATAGTCT	CCGCCTCGTT	CGTCTATGGT	ATGCATCCCA
5110	5120	5130	5140	5150	5160
TTCATTTTCT	TCTTCTGATT	ATTGTCATCT	TTCCCTTTGC	CAAATGGGCA	GTTATTGTTT
5170	5180	5190	5200	5210	5220
CAGGGAGAGA	AGCTGCTCAT	TGGCCAATCA	TTCTGGTGTG	CAGTGCTCCA	TCGGATTCTA
5230	5240	5250	5260	5270	5280
CATGTCCAAC	AAGGCATGTC	TGGATGATGC	AATGTCTGTC	TGACCCCCGG	AATCCGTGTC

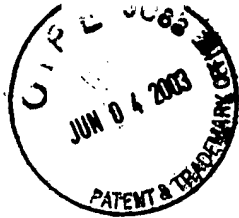
FIG. 11F



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5290	5300	5310	5320	5330	5340
AGAGACAACA	TTCTAGACAG	ATATACACTT	TTTATTATTA	ACAAACTTTG	GCCACAACCT
5350	5360	5370	5380	5390	5400
TTGATGTATA	AATTGCCGGA	TTTCCCCAGT	CCTTTCATTG	TGGCTTTGGA	CAGGAGCAGG
5410	5420	5430	5440	5450	5460
CTCACTTGTC	TGCTTCAGGC	TGCCTTTCTC	TTGGGTTGCA	CCTCAGTTCT	TACTTATTTA
5470	5480	5490	5500	5510	5520
TTTATTTTGA	GTGGAGCATA	GGGGCCTCTT	CCAAAATGGG	TAGAGCTCAG	GGGCTTTCTT
5530	5540	5550	5560	5570	5580
ATTGAAATGG	TCACATGATA	AAAACGGGCT	GAAAAAGGAG	AGTTCCAGGA	GAAAAGCCCA
5590	5600	5610	5620	5630	5640
GAAAAGGCC	CTCCTCAGAA	GACAGCCTTT	AAGCCTCTTG	CTTACTGAAG	GAAGCCCCAC
5650	5660	5670	5680	5690	5700
CTTCTAGCAC	TGAGGCCGGG	TCTGATCTTC	CAGAGGAGTT	GGAGGAGTCC	ATGAGAATGG
5710	5720	5730	5740	5750	5760
CCACCATTCT	TGCTTGCTGC	TGCTGATGTT	GCAGTTTTGA	GAGAACAGCG	GGATCCTTGT
5770	5780	5790	5800	5810	5820
TGTCCTCTAG	AGACTTGAGT	CTGTCACTGA	CATTTTTTCA	GTTTCTTTGC	TCATAGACCA
5830	5840	5850	5860	5870	5880
TACGAGGAAT	TAGTGATGTG	TCAGTTGAGA	GTTTCAATC	TCATTGTTCA	TTTAATTCAC
5890	5900	5910	5920	5930	5940
TTTAAAGTTG	TCAATTTCTG	TGTGAGTAAC	CTGTAAAAGA	CACCTTTCCA	GAAGAGTTTT
5950	5960	5970	5980	5990	6000
GCCGTCTGTT	TGAAAAAAA	ATCTTTATAA	ACTTTCCTAA	GTATCTGGAT	TTGGATTCTT
6010	6020	6030	6040	6050	6060
TATTTGGAGA	GAAAATGTAC	CCTGTCTCCA	CCAAAAATAC	AAAAATTAGC	CAGGCTTGGT
6070	6080	6090	6100	6110	6120
GGTGCACACC	GGTAATCCCA	GCAACTCTGG	AGACTAAGGC	AGGAAGAATC	GCTTGACCCA
6130	6140	6150	6160	6170	6180
GGAGGGTCGA	GGCTACAATG	AGTTGAAACC	GCGCCACTGC	ACTCCAGCCT	GGGCGACAGT
6190	6200	6210	6220	6230	6240
GCGAGGCCCT	GTCTCAAAAA	TAAAATAAAA	TAAATAAATA	AATTAGCCAG	ATACTGTGTG
6250	6260	6270	6280	6290	6300
CACGCCTGCA	GTCCCAGCTA	TTCTGGAAGC	TGAGGTGGGA	AGATGGTTAA	GCCTGAGAGG
6310	6320	6330	6340	6350	6360
ACAAAGCTGC	AGTGAGTCAT	GTTTGTCATCA	CTGCACTCCA	GCCTGGGTGA	CAGAGCAAGA
6370	6380	6390	6400	6410	6420
CCCTGTCTAA	AAAACAAAAA	CAGGCCGGGT	GTGGTGGCTC	ATGCCTGCCA	TCCCAGTGCT
6430	6440	6450	6460		
TTGGGAGGCA	GAGGTTGGCA	TAATCCCAGC	GCTCTGGGAA	TTCC	

FIG. 11G



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GGCCGGGGCC GGGCGGGCGG GTCGCGGGGG CAATGCGGGC GCAGGSCCGG GGGCGCCTTC 60
CCC GGCGGCT GCTGCTGCTG CTGGCGCTCT GGGTGCAGGC GGC GCGGCC ATGGGCTATT 120
TCGAGCTGCA GCTGAGCGCG CTGCGGAACG TGAACGGGGA GCTGCTGAGC GGC GCTGCT 180
GTGACGGCGA CGGCCGGACA ACGCGCGCGG GGGGCTGCGG CCACGACGAG TGC GACACCG 240
CTCCTTTACC CTCATCGTGG AGGCCTGGGA CTGGGACAAC GATACCACCC CGAATGAGGA 300
GCTGCTGATC GAGCGAGTGT CGCATGCCGG C ATG ATC AAC CCG GAG GAC CGC 352
Met Ile Asn Pro Glu Asp Arg
1 5
TGG AAG AGC CTG CAC TTC AGC GGC CAC GTG GCG CAC CTG GAG CTG CAG 400
Trp Lys Ser Leu His Phe Ser Gly His Val Ala His Leu Glu Leu Gln
10 15 20
ATC CGC GTG CGC TGC GAC GAG AAC TAC TAC AGC GCC ACT TGC AAC AAG 448
Ile Arg Val Arg Cys Asp Glu Asn Tyr Tyr Ser Ala Thr Cys Asn Lys
25 30 35
TTC TGC CGG CCC CGC AAT GAC TTT TTC GGC CAC TAC ACC TGC GAC CAG 496
Phe Cys Arg Pro Arg Asn Asp Phe Phe Gly His Tyr Thr Cys Asp Gln
40 45 50 55
TAC GGC AAC AAG GCC TGC ATG GAC GGC TGG ATG GGC AAG GAG TGC AAG 544
Tyr Gly Asn Lys Ala Cys Met Asp Gly Trp Met Gly Lys Glu Cys Lys
60 65 70
GAA GCT GTG TGT AAA CAA GGG TGT AAT TTG CTC CAC GGG GGA TGC ACC 592
Glu Ala Val Cys Lys Gln Gly Cys Asn Leu Leu His Gly Gly Cys Thr
75 80 85
GTG CCT GGG GAG TGC AGG TGC AGC TAC GGC TGG CAA GGG AGG TTC TGC 640
Val Pro Gly Glu Cys Arg Cys Ser Tyr Gly Trp Gln Gly Arg Phe Cys
90 95 100
GAT GAG TGT GTC CCC TAC CCC GGC TGC GTG CAT GGC AGT TGT GTG GAG 688
Asp Glu Cys Val Pro Tyr Pro Gly Cys Val His Gly Ser Cys Val Glu
105 110 115
CCC TGG CAG TGC AAC TGT GAG ACC AAC TGG GGC GGC CTG CTC TGT GAC 736
Pro Trp Gln Cys Asn Cys Glu Thr Asn Trp Gly Gly Leu Leu Cys Asp
120 125 130 135
AAA GAC CTG AAC TAC TGT GGC AGC CAC CAC CCC TGC ACC AAC GGA GGC 784
Lys Asp Leu Asn Tyr Cys Gly Ser His His Pro Cys Thr Asn Gly Gly
140 145 150

FIG. 12A



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ACG TGC ATC AAC GCC GAG CCT GAC CAG TAC CGC TGC ACC TGC CCT GAC	832
Thr Cys Ile Asn Ala Glu Pro Asp Gln Tyr Arg Cys Thr Cys Pro Asp	
155 160 165	
GGC TAC TCG GGC AGG AAC TGT GAG AAG GCT GAG CAC GCC TGC ACC TCC	880
Gly Tyr Ser Gly Arg Asn Cys Glu Lys Ala Glu His Ala Cys Thr Ser	
170 175 180	
AAC CCG TGT GCC AAC GGG GGC TCT TGC CAT GAG GTG CCG TCC GGC TTC	928
Asn Pro Cys Ala Asn Gly Gly Ser Cys His Glu Val Pro Ser Gly Phe	
185 190 195	
GAA TGC CAC TGC CCA TCG GGC TGG AGC GGG CCC ACC TGT GCC CTT GAC	976
Glu Cys His Cys Pro Ser Gly Trp Ser Gly Pro Thr Cys Ala Leu Asp	
200 205 210 215	
ATC GAT GAG TGT GCT TCG AAC CCG TGT GCG GCC GGT GGC ACC TGT GTG	1024
Ile Asp Glu Cys Ala Ser Asn Pro Cys Ala Ala Gly Gly Thr Cys Val	
220 225 230	
GAC CAG GTG GAC GGC TTT GAG TGC ATC TGC CCC GAG CAG TGG GTG GGG	1072
Asp Gln Val Asp Gly Phe Glu Cys Ile Cys Pro Glu Gln Trp Val Gly	
235 240 245	
GCC ACC TGC CAG CTG GAC GCC AAT GAG TGT GAA GGG AAG CCA TGC CTT	1120
Ala Thr Cys Gln Leu Asp Ala Asn Glu Cys Glu Gly Lys Pro Cys Leu	
250 255 260	
AAC GCT TTT TCT TGC AAA AAC CTG ATT GGC GGC TAT TAC TGT GAT TGC	1168
Asn Ala Phe Ser Cys Lys Asn Leu Ile Gly Gly Tyr Tyr Cys Asp Cys	
265 270 275	
ATC CCG GGC TGG AAG GGC ATC AAC TGC CAT ATC AAC GTC AAC GAC TGT	1216
Ile Pro Gly Trp Lys Gly Ile Asn Cys His Ile Asn Val Asn Asp Cys	
280 285 290 295	
CGC GGG CAG TGT CAG CAT GGG GGC ACC TGC AAG GAC CTG GTG AAC GGG	1264
Arg Gly Gln Cys Gln His Gly Gly Thr Cys Lys Asp Leu Val Asn Gly	
300 305 310	
TAC CAG TGT GTG TGC CCA CGG GGC TTC GGA GGC CGG CAT TGC GAG CTG	1312
Tyr Gln Cys Val Cys Pro Arg Gly Phe Gly Gly Arg His Cys Glu Leu	
315 320 325	
GAA CGA GAC AAG TGT GCC AGC AGC CCC TGC CAC AGC GGC GGC CTC TGC	1360
Glu Arg Asp Lys Cys Ala Ser Ser Pro Cys His Ser Gly Gly Leu Cys	
330 335 340	
GAG GAC CTG GCC GAC GGC TTC CAC TGC CAC TGC CCC CAG GGC TTC TCC	1408
Glu Asp Leu Ala Asp Gly Phe His Cys His Cys Pro Gln Gly Phe Ser	
345 350 355	

FIG. 12B



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GGG CCT CTC TGT GAG GTG GAT GTC GAC CTT TGT GAG CCA AGC CCC TGC 1456
Gly Pro Leu Cys Glu Val Asp Val Asp Leu Cys Glu Pro Ser Pro Cys
360 365 370 375
CGG AAC GGC GCT CGC TGC TAT AAC CTG GAG GGT GAC TAT TAC TGC GCC 1504
Arg Asn Gly Ala Arg Cys Tyr Asn Leu Glu Gly Asp Tyr Tyr Cys Ala
380 385 390
TGC CCT GAT GAC TTT GGT GGC AAG AAC TGC TCC GTG CCC CGC GAG CCG 1552
Cys Pro Asp Asp Phe Gly Gly Lys Asn Cys Ser Val Pro Arg Glu Pro
395 400 405
TGC CCT GGC GGG GCC TGC AGA GTG ATC GAT GGC TGC GGG TCA GAC GCG 1600
Cys Pro Gly Gly Ala Cys Arg Val Ile Asp Gly Cys Gly Ser Asp Ala
410 415 420
GGG CCT GGG ATG CCT GGC ACA GCA GCC TCC GGC GTG TGT GGC CCC CAT 1648
Gly Pro Gly Met Pro Gly Thr Ala Ala Ser Gly Val Cys Gly Pro His
425 430 435
GGA CGC TGC GTC AGC CAG CCA GGG GGC AAC TTT TCC TGC ATC TGT GAC 1696
Gly Arg Cys Val Ser Gln Pro Gly Gly Asn Phe Ser Cys Ile Cys Asp
440 445 450 455
AGT GGC TTT ACT GGC ACC TAC TGC CAT GAG AAC ATT GAC GAC TGC CTG 1744
Ser Gly Phe Thr Gly Thr Tyr Cys His Glu Asn Ile Asp Asp Cys Leu
460 465 470
GGC CAG CCC TGC CGC AAT GGG GGC ACA TGC ATC GAT GAG GTG GAC GCC 1792
Gly Gln Pro Cys Arg Asn Gly Gly Thr Cys Ile Asp Glu Val Asp Ala
475 480 485
TTC CGC TGC TTC TGC CCC AGC GGT TGG GAG GGC GAG CTC TGC GAC ACC 1840
Phe Arg Cys Phe Cys Pro Ser Gly Trp Glu Gly Glu Leu Cys Asp Thr
490 495 500
AAT CCC AAC GAC TGC CTT CCC GAT CCC TGC CAC AGC CGC GGC CGC TGC 1888
Asn Pro Asn Asp Cys Leu Pro Asp Pro Cys His Ser Arg Gly Arg Cys
505 510 515
TAC GAC CTG GTC AAT GAC TTC TAC TGT GCG TGC GAC GAC GGC TGG AAG 1936
Tyr Asp Leu Val Asn Asp Phe Tyr Cys Ala Cys Asp Asp Gly Trp Lys
520 525 530 535
GGC AAG ACC TGC CAC TCA CGC GAG TTC CAG TGC GAT GCC TAC ACC TGC 1984
Gly Lys Thr Cys His Ser Arg Glu Phe Gln Cys Asp Ala Tyr Thr Cys
540 545 550
AGC AAC GGT GGC ACC TGC TAC GAC AGC GGC GAC ACC TTC CGC TGC GCC 2032
Ser Asn Gly Gly Thr Cys Tyr Asp Ser Gly Asp Thr Phe Arg Cys Ala
555 560 565
TGC CCC CCC GGC TGG AAG GGC AGC ACC TGC GCC GTC GCC AAG AAC AGC 2080
Cys Pro Pro Gly Trp Lys Gly Ser Thr Cys Ala Val Ala Lys Asn Ser
570 575 580

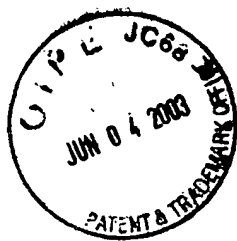
FIG. 12C



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AGC TGC CTG CCC AAC CCC TGT GTG AAT GGT GGC ACC TGC GTG GGC AGC	2128
Ser Cys Leu Pro Asn Pro Cys Val Asn Gly Gly Thr Cys Val Gly Ser	
585 590 595	
GGG GCC TCC TTC TCC TGC ATC TGC CGG GAC GGC TGG GAG GGT CGT ACT	2176
Gly Ala Ser Phe Ser Cys Ile Cys Arg Asp Gly Trp Glu Gly Arg Thr	
600 605 610 615	
TGC ACT CAC AAT ACC AAC GAC TGC AAC CCT CTG CCT TGC TAC AAT GGT	2224
Cys Thr His Asn Thr Asn Asp Cys Asn Pro Leu Pro Cys Tyr Asn Gly	
620 625 630	
GGC ATC TGT GTT GAC GGC GTC AAC TGG TTC CGC TGC GAG TGT GCA CCT	2272
Gly Ile Cys Val Asp Gly Val Asn Trp Phe Arg Cys Glu Cys Ala Pro	
635 640 645	
GGC TTC GCG GGG CCT GAC TGC CGC ATC AAC ATC GAC GAG TGC CAG TCC	2320
Gly Phe Ala Gly Pro Asp Cys Arg Ile Asn Ile Asp Glu Cys Gln Ser	
650 655 660	
TCG CCC TGT GCC TAC GGG GCC ACG TGT GTG GAT GAG ATC AAC GGG TAT	2368
Ser Pro Cys Ala Tyr Gly Ala Thr Cys Val Asp Glu Ile Asn Gly Tyr	
665 670 675	
CGC TGT AGC TGC CCA CCC GGC CGA GCC GGC CCC CGG TGC CAG GAA GTG	2416
Arg Cys Ser Cys Pro Pro Gly Arg Ala Gly Pro Arg Cys Gln Glu Val	
680 685 690 695	
ATC GGG TTC GGG AGA TCC TGC TGG TCC CGG GGC ACT CCG TTC CCA CAC	2464
Ile Gly Phe Gly Arg Ser Cys Trp Ser Arg Gly Thr Pro Phe Pro His	
700 705 710	
GGA AGC TCC TGG GTG GAA GAC TGC AAC AGC TGC CGC TGC CTG GAT GGC	2512
Gly Ser Ser Trp Val Glu Asp Cys Asn Ser Cys Arg Cys Leu Asp Gly	
715 720 725	
CGC CGT GAC TGC AGC AAG GTG TGG TGC GGA TGG AAG CCT TGT CTG CTG	2560
Arg Arg Asp Cys Ser Lys Val Trp Cys Gly Trp Lys Pro Cys Leu Leu	
730 735 740	
GCC GGC CAG CCC GAG GCC CTG AGC GCC CAG TGC CCA CTG GGG CAA AGG	2608
Ala Gly Gln Pro Glu Ala Leu Ser Ala Gln Cys Pro Leu Gly Gln Arg	
745 750 755	
TGC CTG GAG AAG GCC CCA GGC CAG TGT CTG CGA CCA CCC TGT GAG GCC	2656
Cys Leu Glu Lys Ala Pro Gly Gln Cys Leu Arg Pro Pro Cys Glu Ala	
760 765 770 775	
TGG GGG GAG TGC GGC GCA GAA GAG CCA CCG AGC ACC CCC TGC CTG CCA	2704
Trp Gly Glu Cys Gly Ala Glu Glu Pro Pro Ser Thr Pro Cys Leu Pro	
780 785 790	
CGC TCC GGC CAC CTG GAC AAT AAC TGT GCC CGC CTC ACC TTG CAT TTC	2752
Arg Ser Gly His Leu Asp Asn Asn Cys Ala Arg Leu Thr Leu His Phe	
795 800 805	

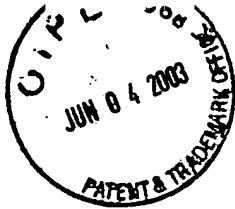
FIG. 12D



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AAC CGT GAC CAC GTG CCC CAG GGC ACC ACG GTG GGC GCC ATT TGC TCC	2800
Asn Arg Asp His Val Pro Gln Gly Thr Thr Val Gly Ala Ile Cys Ser	
810 815 820	
GGG ATC CGC TCC CTG CCA GCC ACA AGG GCT GTG GCA CGG GAC CGC CTG	2848
Gly Ile Arg Ser Leu Pro Ala Thr Arg Ala Val Ala Arg Asp Arg Leu	
825 830 835	
CTG GTG TTG CTT TGC GAC CGG GCG TCC TCG GGG GCC AGT GCT GTG GAG	2896
Leu Val Leu Leu Cys Asp Arg Ala Ser Ser Gly Ala Ser Ala Val Glu	
840 845 850 855	
GTG GCC GTG TCC TTC AGC CCT GCC AGG GAC CTG CCT GAC AGC AGC CTG	2944
Val Ala Val Ser Phe Ser Pro Ala Arg Asp Leu Pro Asp Ser Ser Leu	
860 865 870	
ATC CAG GGC GCG GCC CAC GCC ATC GTG GCC GCC ATC ACC CAG CGG GGG	2992
Ile Gln Gly Ala Ala His Ala Ile Val Ala Ala Ile Thr Gln Arg Gly	
875 880 885	
AAC AGC TCA CTG CTC CTG GCT GTC ACC GAG GTC AAG GTG GAG ACG GTT	3040
Asn Ser Ser Leu Leu Leu Ala Val Thr Glu Val Lys Val Glu Thr Val	
890 895 900	
GTT ACG GGC GGC TCT TCC ACA GGT CTG CTG GTG CCT GTG CTG TGT GGT	3088
Val Thr Gly Gly Ser Ser Thr Gly Leu Leu Val Pro Val Leu Cys Gly	
905 910 915	
GCC TTC AGC GTG CTG TGG CTG GCG TGC GTG GTC CTG TGC GTG TGG TGG	3136
Ala Phe Ser Val Leu Trp Leu Ala Cys Val Val Leu Cys Val Trp Trp	
920 925 930 935	
ACA CGC AAG CGC AGG AAA GAG CGG GAG AGG AGC CGG CTG CCG CGG GAG	3184
Thr Arg Lys Arg Arg Lys Glu Arg Glu Arg Ser Arg Leu Pro Arg Glu	
940 945 950	
GAG AGC GCC AAC AAC CAG TGG GCC CCG CTC AAC CCC ATC CGC AAC CCC	3232
Glu Ser Ala Asn Asn Gln Trp Ala Pro Leu Asn Pro Ile Arg Asn Pro	
955 960 965	
ATT GAG CGG CCG GGG GGG CAC AAG GAC GTG CTC TAC CAG TGC AAG AAC	3280
Ile Glu Arg Pro Gly Gly His Lys Asp Val Leu Tyr Gln Cys Lys Asn	
970 975 980	
TTC ACT CCA CCG CCG CGC AGG CGC TGC CCG GGC CGG CCG GCC ACG CGG	3328
Phe Thr Pro Pro Pro Arg Arg Cys Pro Gly Arg Pro Ala Thr Arg	
985 990 995	
CCG TCA GGG AGG ATG AGG AGG ACG AGG ATC TTG GCC GCG GTG AGG AGG	3376
Pro Ser Gly Arg Met Arg Arg Thr Arg Ile Leu Ala Ala Val Arg Arg	
1000 1005 1010 1015	
ACT CCC TGG AGG CGG AGA AGT TCC TCT CAC ACA AAT TCA CCA AAG ATC	3424
Thr Pro Trp Arg Arg Arg Ser Ser Ser His Thr Asn Ser Pro Lys Ile	
1020 1025 1030	

FIG. 12E



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CTG GCC GCT CGC CGG GGA GGC CGG CCC ACT GGG CCT CAG GCC CCA AAG 3472
Leu Ala Ala Arg Arg Gly Gly Arg Pro Thr Gly Pro Gln Ala Pro Lys
1035 1040 1045
TGG ACA ACC GCG CGG TCA GGA GCA TCA ATG AGG CCC GCT ACG TCG GCA 3520
Trp Thr Thr Ala Arg Ser Gly Ala Ser Met Arg Pro Ala Thr Ser Ala
1050 1055 1060
AGG GAA GTA GGG CGG CTG CAG CTG GGC CGG GAC CCA GGG CCC TCG GTG 3568
Arg Glu Val Gly Arg Leu Gln Leu Gly Arg Asp Pro Gly Pro Ser Val
1065 1070 1075
GGA GCC ATG CCG TCT GCC GGA CCC GGA GGC CGA GGC CAT GTG CAT AGT 3616
Gly Ala Met Pro Ser Ala Gly Pro Gly Gly Arg Gly His Val His Ser
1080 1085 1090 1095
TTC TTT ATT TTG TGT AAA AAA ACC ACC AAA AAC AAA AAC CAA ATG TTT 3664
Phe Phe Ile Leu Cys Lys Lys Thr Thr Lys Asn Lys Asn Gln Met Phe
1100 1105 1110
ATT TTC TAC GTT TCT TTA ACC TTG TAT AAA TTA TTC AGT AAC TGT CAG 3712
Ile Phe Tyr Val Ser Leu Thr Leu Tyr Lys Leu Phe Ser Asn Cys Gln
1115 1120 1125
GCT GAA AAC AAT GGA GTA TTC TCG GAT AGT TGC TAT TTT TGT AAA GTA 3760
Ala Glu Asn Asn Gly Val Phe Ser Asp Ser Cys Tyr Phe Cys Lys Val
1130 1135 1140
GCC GTG CGT GGC ACT CGC TGT ATG AAA GGA GAG AGC AAA GGG TGT CTG 3808
Ala Val Arg Gly Thr Arg Cys Met Lys Gly Glu Ser Lys Gly Cys Leu
1145 1150 1155
CGT CGT CAC CAA ATC GTC GCG TTT GTT ACC AGA GGT TGT GCA CTG TTT 3856
Arg Arg His Gln Ile Val Ala Phe Val Thr Arg Gly Cys Ala Leu Phe
1160 1165 1170 1175
ACA GAA TCT TCC TTT TAT TCC TCA CTC GGG TTT CTC TGT GCT CCA GGC 3904
Thr Glu Ser Ser Phe Tyr Ser Ser Leu Gly Phe Leu Cys Ala Pro Gly
1180 1185 1190
CAA AGT GCC GGT GAG ACC CAT GGC TGT GTT GGT GTG GCC CAT GGC TGT 3952
Gln Ser Ala Gly Glu Thr His Gly Cys Val Gly Val Ala His Gly Cys
1195 1200 1205
TGG TGG GAC CCG TGG CTG ATG GTG TGG CCT GTG GCT GTC GGT GGG ACT 4000
Trp Trp Asp Pro Trp Leu Met Val Trp Pro Val Ala Val Gly Gly Thr
1210 1215 1220
CGT GGC TGT CAA TGG GAC CTG TGG CTG TCG GTG GGA CCT ACG GTG GTC 4048
Arg Gly Cys Gln Trp Asp Leu Trp Leu Ser Val Gly Pro Thr Val Val
1225 1230 1235

FIG. 12F



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GGT GGG ACC CTG GTT ATT GAT GTG GCC CTG GCT GCC GGC ACG GCC CGT 4096
Gly Gly Thr Leu Val Ile Asp Val Ala Leu Ala Ala Gly Thr Ala Arg
1240 1245 1250 1255
GGC TGT TG ACGCACCTGT GGTGTGTTAGT GGGGCCTGAG GTCATCGGCG TGGCCCAAGG 4154
Gly Cys
CCGGCAGGTC AACCTCGGCG TTGCTGGCCA GTCCACCCTG CCTGCCGTCT GTGCTTCCTC 4214
CTGCCCAGAA CGCCCGCTCC AGCGATCTCT CCACTGTGCT TTCAGAAGTG CCCTTCCTGC 4274
TGCGCAGTTC TCCCATCCTG GGACGGCGGC AGTATTGAAG CTCGTGACAA GTGCCTTCAC 4334
ACAGACCCCT CGCAACTGTC CACGCGTGCC GTGGCACCAG GCGCTGCCCA CCTGCCGGCC 4394
CCGGCCGCCC CTCCTCGTGA AAGTGCATTT TTGTAAATGT GTACATATTA AAGGAAGCAC 4454
TCTGTATAAA AAAAAAAAAAC CGGAATTCC 4483

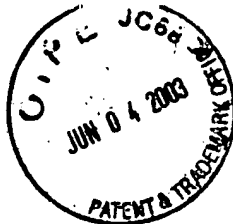
FIG. 12G



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CAGGTGGCGTCAGCATCGGGACAGTTCGAGCTGGAGATCTTATCCGTGCAGAATGTGAACGGCGTGCT
GCAGAACGGGAACCTGCTGCGACGGCACTCGAAACCCCGGAGATAAAAAAGTGCACCAGAGATGAGTGTG
ACACCTACTTTAAAGTTTGCCTGAAGGAGTACCACTCGCGGGTCACTGCTGGCGGCCCTTGCAGCTTC
GGATCCAAATCCACCCCTGTCATCGGCGGGAATACCTTCAATTTAAAGTACAGCCGGAATAATGAAAA
GAACCGGATTGTTATCCCTTTCACGTTGCGCTGGCCGAGATCCTACACGTTGCTTGTGAGGCATGGG
ATTACAATGATAACTCTACTAATCCCGATCGCATAATTGAGAAGGCATCCCACTCTGGCATGATCAAT
CCAAGCCGTCACTGGCAGACGTTGAAACATAACACAGGAGCTGCCCACTTTGAGTATCAAATCCGTGT
GACTTGGCGCAGAACATTACTATGGCTTTGGATGCAACAAGTTTTGTGACCGAGAGATGACTTCTTCA
CTCACCATACTGTGACCAGAATGGCAACAAAACCTGCTTGGAAAGGCTGGACGGGACCAGAATGCAAC
AAAGCTATTTGTGTCAGGGATGTAGCCCCAAGCATGGTTCTTGCACAGTTCAGGAGAGTGCAGGTG
TCAGTATGGATGGCAAGGCCAGTACTGTGATAAGTGCATTCCACACCCGGGATGTGTCCATGGCACTT
GCATTGAACCATGGCAGTGCCTCTGTGAAACCACTGGGGTGGTCAGCTCTGTGACAAAGACCTGAAC
TACTGTGGAACCCACCCACCTGTTTGAATGGTGGTACCTGCAGCAACACTGGCCCCGATAAATACCA
GTGTTCCCTGCCCTGAGGGTTACTCAGGACAGAAGTGTGAAATAGCGGAGCATGCGTGCCTCTCTGATC
CGTGCCACAACGGAGGAAGCTGCCTAGAAACGTCTACAGGATTTGAATGTGTGTGTGCACCTGGCTGG
GCTGGACCAACTTGCACTGATAATATTGATGATTGTTCTCCAAATCCCTGTGGTCATGGAGGAACCTG
CCAAGATCTAGTTGATGGATTTAAGTGTATTTGCCACCTCAGTGGACTGGCAAAACATGCCAGCTAG
ATGCGAATGAATGTGAGGGCAAACCTGTGTCAATGCCAATCCTGCAGGAACCTTGATTGGCAGCTAC
TATTGTGACTGCATTACTGGTGGTCTGGCCACAAGTGTGATATAAATATTAATGATTGTGCTGGACA
ATGTCAGAATGGAGGATCCTGTGCGGACTTGGTTAATGGTTATCGGTGCATCTGTTACCTGGCTATG
CAGGAGATCACTGTGAGAAAGACATCAATGAATGTGCAAGTAACCCCTTGATGAATGGGGGTCACTGC
CAGGATGAAATCAATGGATTCCAATGTCTGTGCTGCTGGTTTCTCAGGAAACCTCTGTGAGCTGGA
TATAGACTACTGTGAGCCAAACCTTGCCAGAACGGTGCCAGTGCTTCAATCTTGCTATGGACTATT
TCTGTAAGTGCCTGAAGATTACGAAGGCAAGAACTGCTCCACCTGAAAGATCACTGCCGCACAAGT
CCTTGTGAAGTAATCGACAGCTGTACAGTGGCAGTGGCTTCTAACAGCACACCAGAAGGAGTTGTTA
CATTTCTTCAAATGTCTGTGGTCCCTCATGGAAAAAGCAAGAGCCAAGCAGGTGGAAAAATTCACCTGTG
AATGCAACAAAGGATTCACTGGCACCTACTGTGATGAGAATATCAATGACTGTGAGAGCAACCCCTGT
AAAAATGGTGGCACTTGTATTGACGGTGTAACTCCTACAAATGTATTTGTAGTGATGGATGGGAAGG
AACATATTGTGAAACAAATATTAATGACTGCAGTAAAAACCCCTGCCACAATGGAGGAACCTTGCCGAG
ACTTGGTCAATGACTTCTTCTGTGAATGTAAAAATGGGTGGAAAGGAAAAATTTGCCACTCTCGTGAC
AGCCAGTGTGATGAGGCAACATGCAATAATGGAGGAACATGTTATGATGAGGGGGACACTTTCAAGTG
CATGTGTCTGTCAGGATGGGAAGGAGCCACTTGTAAATAGCAAGGAACAGCAGCTGCCTGCCAAACC
CCTGTCACAATGGTGGTACCTGTGTAGTTAGTGGGGATTCTTTCACCTGTGTCTGCAAGGAGGGCTGG
GAAGGACCGACATGTACTCAGAACACAATGACTGCAGTCTCATCCTTGTACAACAGTGGTACTTG
TGTTGATGGAGACAACCTGGTACCGCTGTGAGTGCCTCCCGGCTTCGAGGTCCCGACTGTAGGATCA
ACATCAATGAATGTGAGTCTTACCCTGTGCCTTTGGGGCTACTTGTGTGGATGAAATTAATGGGTAC
CGTTGCATTTGTCCACCGGGTGCAGTGGTCCAGGATGCCAGGAAGTTACAGGGAGGCCTTGCTTTAC
CAGTATTCGAGTAATGCCAGACGGTGTAAAGTGGGATGATGACTGTAATACTTGTGAGTGTGTAATG
GAAAAGTCACCTGTTCTAAGGTTTGGTGTGGTCTCGACCTTGTATAATACATGCCAAAGGTCATAAT
GAATGCCACAGCTGGACACGCTTGTGTTCTGTAAAGAAGACCATTGTTTCACTCATCCTTGTGCTGC

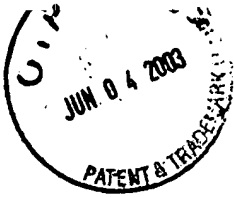
FIG. 13A



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AGTGGGTGAATGCTGGCCTTCTAATCAGCAGCCTGTGAAGACCAAATGCAATTCTGATTCTTATTACC
AAGATAATTGTGCCAACATCACCTTCACCTTTAATAAGGAAATGATGGCACCAGGCCTTACCACGGAG
CACATTTGCAGTGAATTGAGGAATCTGAATATCCTGAAGAATGTTTCTGCTGAATATTCCATCTATAT
TACCTGTGAGCCTTCACACTTGGCAAATAATGAAATACATGTTGCTATTTCTGCTGAAGATATAGGAG
AAGATGAAAACCCAATCAAGGAAATCACAGATAAGATTATTGACCTTGTCAGTAAGCGTGATGGAAAC
AACACACTAATTGCTGCAGTCGCAGAAGTCAGAGTACAAAGGCGACCAGTTAAGAACAAAACAGATTT
CTTGGTGCCATTACTGAGCTCAGCTTAACAGTAGCCTGGATCTGCTGTCTGGTAACTGTTTTCTATT
GGTGCAATCAAAAGCGCAGAAAGCAGAGCAGCCATACTCACACAGCATCTGATGACAACACCACCAAC
AACGTAAGGGAGCAGCTGAATCAGATTA AAAACCCCATAGAGAAACACGGAGCAAATACTGTTCCAAT
TAAAGACTATGAAAACAAAACTCTAAAAATCGCCAAAATAAGGACGCACAATTCAGAAGTGGAGGAAG
ATGACATGGACAAACACCAGCAAAAGGCCCGGTTTGCCAAGCAGCCAGCGTACACTTTGGTAGACAGA
GATGAAAAGCCACCCAACAGCACACCCACAAAACACCCAACTGGACAAATAAACAGGACAACAGAGA
CTTGGAAGTGCACAAAGTTTAAATAGAATGGAGTACATTGTATAG

FIG. 13B



QVASASGQFE LEILSVQNVN GVLQNGNCCD GTRNPGDKKC TRDECDTYFK 50
VCLKEYQSRV TAGGPCSFGS KSTPVIGGNT FNLKYSRNE KNRIVIPFSF 100
AWPRSYTLLV EAWDYNDNST NPDRIIEKAS HSGMINPSRQ WQTLKHNTGA 150
AHFEYQIRVT CAEHYYGFGC NKFCRPRDDF FTEHTCDQNG NKTCLGWTG 200
*****DSL DOMAIN*****
PECNKAICRQ GCSPKHGSCV VPGECCQYG WQGQYCDKCI PHPGCVHGTG 250
*** <-----EGF 1----->-----
IEPWQCLCET NWGGQLCDKD LNYCGTHPPC LNGGTCSNTG PDKYQCSCPE 300
-----EGF 2----->-----EGF 3-----
GYSGQNCIEA EHACLSDPCH NGGSCLETST GFECVCAPGW AGPTCTDNID 350
----->-----EGF 4-----
DCSPNPCGHG GTCQDLVDGF KCICPPQWTG KTCQLDANEC EGKPCVNANS 400
>-----EGF 5----->-----
CRNLIGSYYC DCITGWSGHN CDININDCRG QCQNGGSCRD LVNGYRCICS 450
-----EGF 6----->-----EGF 7-----
PGYAGDHCEK DINECASNPC MNGGHCQDEI NGFQCLCPAG FSGNLCQLDI 500
----->-----EGF 8-----
DYCEPNPCQN GAQCFNLAMD YFCNCPEDYE GKNCSHLKDQ CRTTPCEVID 550
>-----EGF 9----->-----
SCTVAVASNS TPEGVRYISS NVCGPHGKCK SQAGGKFTCE CNKGFTGTYC 600
-----EGF 10-----
HENINDCESN PCKNGGTCID GVNSYKCICS DGWEGTYCET NINDCSKNPC 650
----->-----EGF 11----->-----
HNGGTCRDLV NDFFCECKNG WKGKCHSRD SQDEATCNN GGTCYDEGDT 700
-----EGF 12----->-----
FKCMCPAGWE GATCNIARNS SCLPNPCHNG GTCVVS GDSF TCVCKEGWEG 750
EGF 13----->-----EGF 14-----
PTCTQNTNDC SPHPCYNSGT CVDGDMWYRC ECAPGFAGPD CRININECQS 800
----->-----EGF 15----->-----
SPCAFGATCV DEINGYRCIC PPGRSGPGCQ EVTGRPCFTS IRVMPDGAKW 850
-----EGF 16----->-----
DDDCNTCQCL NGKVTCSKVW CGPRPCIHA KGHNECPAGH ACVPVKEDHC 900
<----- CYSTEINE-RICH REGION
FTHPCAAGE CWPSNQPVK TKCNSDSYYQ DNCANITFTF NKEMMAPGLT 950
>-----
TEHICSELRN LNILKNVSAE YSIYITCEPS HLANNEIHVA ISAEDIGEDE 1000

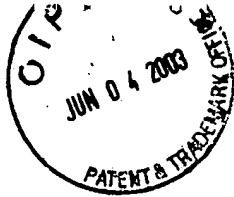
FIG. 14A



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NPIKEITDKI IDLVSKRDGN NTLIAAAEV RVQRRPVKNK TDFLVPLLSS 1050
VLTVAWICCL VTVFYWCIQK RRKQSSHTHT ASDDNTNNV REQLNQIKNP 1100
IEKHGANTVP IKDYENKNSK IAKIRTHNSE VEEDMDKHQ QKARFAKQPA 1150
YTLVDRDEKP PNSTPTKHPN WTNKQDNRL ESAQSLNRME YIV 1193

FIG. 14B



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GAATTCGGCACGAGGTTTTTTTTTTTTTCCCTCTTTCTTTCTTTCTTTTGCC
-----+-----+-----+-----+-----+-----+ 60

61 ATCCGAAAGAGCTGTCAGCCGCCGCCGGCTGCACCTAAAGGCGTCGGTAGGGGGATAAC
-----+-----+-----+-----+-----+-----+ 120

121 AGTCAGAGACCTCCTGAAAGCAGGAGACGGACGGTACCCCTCCGGCTCTGCGGGGCGG
-----+-----+-----+-----+-----+-----+ 180

181 CTGCGGCCCCCTCCGTTCTTTCCCTCCCGAGAGACACTCTTCTTTCCCCCACGAAG
-----+-----+-----+-----+-----+-----+ 240

241 ACACAGGGGCAGGAACGCGAGCGCTGCCCTCCGCCATGGGAGGCCGCTTCTGCTGACG
-----+-----+-----+-----+-----+-----+ 300

301 CTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGCTCCGGGTGTTGAG
-----+-----+-----+-----+-----+-----+ 360

361 CTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGCTGCTCAGCAACCGCAACTGCTGCCGG
-----+-----+-----+-----+-----+-----+ 420

421 GGGGGCGGCCCCGAGGCGCCGGGCAGCAGCAGTGCAGTCAAGACCTTCTTCGCGTC
-----+-----+-----+-----+-----+-----+ 480

481 TGCCTGAAGCACTACCAGGCCAGCGTCTCCCCGAGCCGCCCTGCACCTACGGCAGCGCC
-----+-----+-----+-----+-----+-----+ 540

541 ATCACCCCGTCCTCGGCGCAACTCCTTCAGCGTCCCCGACGGCGGGCGGGCGCCGAC
-----+-----+-----+-----+-----+-----+ 600

601 CCCGCCTTCAGCAACCCCATCCGCTTCCCTTCGGCTTACCTGGCCCGGCACCTTCTCG
-----+-----+-----+-----+-----+-----+ 660

661 CTCATCATCGAGGCTCTGCACACCGACTCCCCGACGACCTACCACAGAAAACCCCGAG
-----+-----+-----+-----+-----+-----+ 720

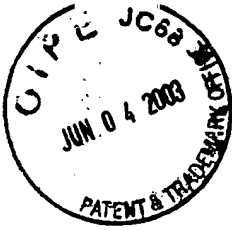
721 CGCCTCATCAGCCGCTGGCCACCCAGAGGCACCTGGCGGTGGGCGAGGAGTGGTCCCAG
-----+-----+-----+-----+-----+-----+ 780

781 GACCTGCACAGCAGCGGCCGACCGACCTCAAGTACTCCTATCGCTTTGTGTGTATGAG
-----+-----+-----+-----+-----+-----+ 840

FIG. 15A



FIG. 15B



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GTCAACGACTACTCCTGCACCTGCCCCCGGGATACAACGGGAAGAACTGCAGCACGCCG
1681 -----+-----+-----+-----+-----+-----+ 1740

GTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGAAGCAAC
1741 -----+-----+-----+-----+-----+-----+ 1800

CGCTACGTGTGCGAGTGCCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCC
1801 -----+-----+-----+-----+-----+-----+ 1860

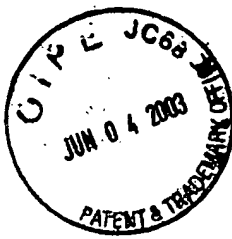
GAGCCACCTCAGGGGCGGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAAC
1861 -----+-----+-----+-----+-----+-----+ 1920

AGCCAGTTTCCCTGGATCGCAGTGTGCGCCGGGATTATTCTGCTCCTCATGCTGCTGCTG
1921 -----+-----+-----+-----+-----+-----+ 1980

TACCAGTCGGTGTACGTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTG
2401 -----+-----+-----+-----+-----+-----+ 2460

TAAAACAGACGTGACGTGGCAAAGCTTATCGATACCGTCATCAAGCTT
2461 -----+-----+-----+-----+-----+-----+ 2508

FIG. 15C



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1 GAATCGGCACGAGGTTTTTTTTTTTTTTTTTTTTTCCCTCTTTTCTTTCTTTTCCCTATCCGAAG 69
70 AGCTGTAGCGCGCGGGCTGCACCTAAGGGCTCGGTAGGGGATAACAGTCAGAGACCTCCTGA 138
139 AAGCAGGAGACGGGACGGTACCCCTCGGCTCTGGGGGGGCTGGGGCCCTCGGTTCTTCCCCCTC 207
208 CCCGAGAGACACTCTTCTTTCCCCCAGGAAGACACAGGGGAGGAACGAGCGGTGCCCTCCGCC 276
277 ATGGAGGCGCTTCTGTGACGCTGCCCTCCTCTGGGGCTGTGTGGGCTGCCAGGTGACGGC 345
346 TCCGGGTGTTGAGCTGAAGCTGCAGGAGTTGTCAACAAGAAGGGCTGCTCAGCAACCGCACTGC 414
415 TGCCGGGGGGCGGCCCGGAGGGCGCGGGCAGCAGTGCGACTGCAAGACCTTCTTCCGGCTCTGC 483
484 CTGAAGCACTACAGGCCAGCGTCTCCCGAGCGCCCTGACCTACGGCAGGCCATACCCCGTGC 552
553 CTGGCGGCAACTCTTTCAGCGTCCCCGAGCGGGCGGGCGCCGACCCCGCTTCAGCAACCCATC 621
622 CGTTCCCTTCGGCTTCACTGGCCCGGCACTTCTCGTCTATCATCGAGGCTTCGACACCGACTCC 690
691 CCCGACGACTCACACAGAAACCCCGAGCGCTCATCAGCGCTTGGCCACCCAGAGGCACTGGCG 759
760 GTGGCGAGGAGTGTCCAGGACCTGCACAGCGGGCGCACCGACCTCAAGTACTCTATCGCTTT 828
829 XXGTGTATGAGCACTACTACGGGGAAGGCTGTGTCTTCTGCGGGCCCGTGACGACCGCTTCGGT 897
898 CACTTCACCTGTGGAGAGCGTGGCGAGAAGGTTCGAACCGAGGCTGGAAGGGCAGTACTGCAGT 966
967 CCGATTGCTTGGCTGGGTGTGACGAGCAGCAGCGCTTCTGGCAAAACCTGGGGAATGCAAGTGCAG 1035
1036 GTGGGTGGCAGGGGGGCTGTGACGAGTGCATCCGATACCCAGGCTGCTGCAACCAAGGACCTG 1104
1105 CAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGCGGCTTCTGCAACCAAGGACCTGAAC 1173
1174 ACTCACCACAAGCCATGCAAGAAATGGTGCCACATGCACCAACCGGTGAGGGAGCTACACT 1242
1243 TGCCGACCTGGGTACACAGGCTCCAGCTGCGAGATTGAATCAACGAATGTGATGCCAACCTT 1311
1312 AATGGTGAAGCTGCACGGATCTCGAGAACAGCTATTCTGTACTGCCCCCAGGCTTCTATGGT 1380
1381 AACTGTGAGCTGAGTGCAATGACTTGTGTGATGGACCGTGTCTCAATGGAGGGCGATGCAC 1449
1450 CCTGATGGTGGATACAGTGGCGTGGCCCTGCCCCACTGGGTATTCTGGGTCAACTGTGAAA 1518
1519 TACTGCAGTTCAGCCCTTGTGCTAATGGAGCCAGTGGCTTGAACCTGGGAACTCTACATATGC 1587
1588 TGCCAGGCTGGCTTCACTGGCAGGCACTGTGACGACAACGTGGAGGATGGCCCTCCTTCCC 1656
1657 AATGGAGGGACCTGTGAGGATGGGTCAACGACTACTCTGCACCTGCCCCCGGATACAACGG 1725
1726 AACTGCAGCACGCGGTGAGCAGATGCGAGCACACCCCTGCCACAATGGGGCCACTGCCACGAG 1794

FIG. 16A



FIG. 16B



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1 MGRFLLTLA LLSALLCRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG GPGGAGQQQC
61 DCKTFFRVCL KHYQASVSPE PPCTYGSALT PVLGANSFSV PDGAGGADPA FSNPIRFPFG
121 FTWPGTFSLI IEALHTDSPD DLTTENPERL ISRLATQRHL AVGEEWSQDL HSSGRDLYKY
181 SYRFVCDHY YGEGCSVFCR PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPQCDEQ
241 HGFCDKPGEC KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT
301 HHKPCNGAT CTNTGQGSYT CSCRPGYTGS SCEIEINECD ANPCKNGGSC TDLENSYSCT
361 CPPGFYGNKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC PLGYSGFNCE KKIDYCSSSP
421 CANGAQCVDL GNSYICQQA GFTGRHCDN VDDCASFPV NGGTCQDGVN DYSCTCPPGY
481 NGKNCSTPVS RCEHNPCHNG ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT
541 EKYTEGQNSQ FPWIAVCAGI ILVLMLLGC AAIVVCVRLK VQKRHHOPEA CRSETETMNN
601 LANCQREKDI SISVIGATQI KNTNKKVDFH SDNSDKNGYK VRYPVVDYNL VHELKNEDSV
661 KEEHGKCEAK CETYDSEAE KSAVQLKSSD TSEKRPDSV YSTSKDTKYQ SVYVISEEKD
721 ECIIATEV

FIG. 17

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[illegible]

FIG. 18A



C-Delta-1 417 S S P C A N G A Q C V D L G N S Y I C Q C Q A G F T G R H C D D N V D D C A S F P C V N G G T C Q D G V N D Y S C T C P 477
X-Delta-1 412 S S N P C A N G A R C E D L G N S Y I C Q C Q E G P S G R N C D D N L D D C T S F P C Q N G G T C Q D G I N D Y S C T C P 472
Delta 423 S P N P C I N G G S C Q P S G K . . . C I C P S G F S G T R C E T N I D D C L G H Q C E N G G T C T D M V N Q Y R C Q C V 480
EGF6

C-Delta-1 478 P G Y N G K N C S T P V S R C E H N P C H N G A T C H E R S N R Y V C E C A R G Y G G L N C Q F L L P E P P Q G P . . . 534
X-Delta-1 473 P G Y I G K N C S M P I T K C E H N P C H N G A T C H E R N N R Y V C Q C A R G Y G G N N C Q F L L P E . . . 524
Delta 481 P G F H G T H C S S K V D L C L I R P C A N G T C L N L N D Y Q C T C R A G F T G K D C S V D I D E C S S G P C H N G 541
EGF8

C-Delta-1 535 V I V D F T E . . . K Y T E G Q N S Q F P W . . . I A V C A G I I L V L 564
X-Delta-1 525 E K P V V D L T E . . . K Y T E G Q S Q O F P W . . . I A V C A G I V L V L 557
Delta 542 G T C M N R V N S F E C V C A N G F R G K Q C D E E S Y D S V T F D A H Q Y G A T T Q A R A D G L A N A Q V V I I A V F S 602
EGF9

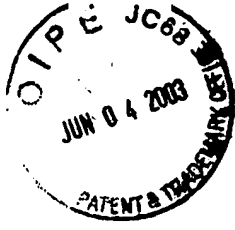
C-Delta-1 565 M L L L G C A A I V V C V R L K V Q K R H Q P E A C R S E T E T M N N L A N C Q R E K D . . . I S I S V I G A T Q I K N T 623
X-Delta-1 558 M L L L G C A A V V V C V R V R V Q K R R H Q P E A C R S E S T M N N L A N C Q R E K D . . . I S V S F I G T T O I K N T 616
Delta 603 V A M P L V A V I A A C V F P C M K R K R K R A Q E K D N A E A R K Q N E Q M A V A T M H H N G S A V G V A L A S A S M G 663
TM

C-Delta-1 624 N K K V D F H S D . N S D K N G Y K V R Y P S V D Y N L V H E L K N E D S V K E E H G K C B A K C B T Y D S E A E E K S A 683
X-Delta-1 617 N K K I D F L S E S N N E K N G Y K P R Y P S V D Y N L V H E L K N E D S P K E E R S K C E A K C S S N D S D S E D V N S 677
Delta 664 G K T G S N S G L T F D G G N P N I K N T W D K S V N . N I C A S A A A A A A A A A A D E C L N Y G G Y V A S V A D N 723

C-Delta-1 684 V Q L K S S D T S E R K R P D S V Y S T S K D T K Y Q S V Y V I S E E K D E C I I A T E V 728
X-Delta-1 678 V H S K . R D S E R R R P D S A Y S T S K D T K Y Q S V Y V I S D E K D E C I I A T E V 721
Delta 724 N N A N S D F C V A P L Q R A K S Q K Q L N T D P T L M H R G S P A G T S A K G A S G G P G A A E G K R I S V L G E G S 784

Delta 785 Y C S Q R W P S L A A A G V A G A C S S Q L M A A S A A G T D G T A Q Q R S V V C G T P H M 832

FIG. 18B



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CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCCATGGGCC GTCGGAGCGC GCTAGCCCTT 60
GCCGTGGTCT CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG 120
CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGAACCGCA ACTGCTGCCG CGGGGCTCT 180
GGCCCGCCTT GCGCTGCAG GACCTTCTTT CCGGTATGCC TCAAGCACTA CCAGGCCAGC 240
GTGTCACCGG AGCCACCCCTG CACCTACGGC AGTGCCGTCA CGCCAGTGCT GGGTGTGAC 300
TCCTTCAGCC TGCCCTGATGG CGCAGGCATC GACCCCGCCT TCAGCAACCC CATCCGATTC 360
CCCTTCGGCT TCACCTGGCC AGGTACCTTC TCTCTGATCA TTGAAGCCCT CCATACAGAC 420
TCTCCCGATG ACCTCGCAAC AGAAACCCCA GAAAGACTCA TCAGCCGCCCT GACCACACAG 480
AGGCACCTCA CTGTGGGAGA AGAATGGTCT CAGGACCTTC ACAGTAGCGG CCGCACAGAC 540
CTCCGGTACT CTTACCGGTT TGTGTGTGAC GAGCACTACT ACGGAGAAGG TTGCTCTGTG 600
TTCTGCCGAC CTCGGGATGA AGGCCAGTAC CACTTCACCT GCGGGGACAG AGGGAGAAG 660
ATGTGCGACC CTGGCTGGAA ATGGATACTG TGACAAACCA GGGGAGTGCA AGTGCAAGT 720
GATGACCAAC ATGGATACTG GCGATGAGTG CATCCGATAC CCAGGTTGTC TCCATGGCAC CTGCCAGCAA 840
GGCCGCTACT GTAAC TGCCA GGAAGGCTGG GGGGGCTTT TCTGCAACCA AGACCTGAAC 900
CCCTGGCAGT ACCATAAGCC GTGCAGGAAT GGAGCCACCT GCACCAACAC GGGCAGGGG 960
TACTGTACTC GTTCCTGCCG CTAGCCCCCTG CAAGAACGGA GCGAGCTGCA CCGACCTTGA GGACAGCTTC 1020
AGCTACACAT GTTCCTGCCG GCGCTCCCGG CTTCTATGGC AAGGCTGTG AGCTGAGCT GGAAGTAGAT 1080
GAGTGTGCTC CTAGCCCCCTG GCGCTCCCGG CTTCTATGGC AAGGCTGTG AGCTGAGCT GGAAGTAGAT 1140
TCTTGACACT GCGCTCCCGG CTTGCTTCAA TGGAGGACGA TGTTCAGATA ACCCTGACGG AGGCTACACC 1200
GCAGATGGCC CCTTGGGCTT CTCTGGGCTT CTCTGGGCTT AACTGTGAGA AGAAGATGGA TCTCTGCGGC 1260
TGCCATTGCC GTTCTAACGG TGCCAAAGTGT GTGGACCTCG GCAACTCTTA CCTGTGCCCG 1320
TCTTCCCTTT GCTTCTCCCG GAGGTACTGC GAGGACAATG TGGATGACTG TGCCTCCTCC 1380

FIG. 19A



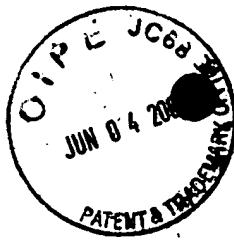
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1440	CCGTGTGCAA	ATGGGGGCAC	CTGCCGGGAC	AGTGTGAACG	ACTTCTCCTG	TACCTGCCCA
1500	CCTGGCTACA	CGGCAAGAA	CTGCAGCGCC	CCTGTACGCA	GGTGTAGCA	TGCACCCCTGC
1560	CATAATGGG	CCACCTGCCA	CCAGAGGGC	CAGCGCTACA	TGTGTAGTG	CGCCACAGGC
1620	TATGGCGGCC	CCAAC TGCCA	GTTTCTGCTC	CCTGAGCCAC	CACCAGGGCC	CATGGTGGTG
1680	GACCTCAGTG	AGAGGCATAT	GGAGAGCCAG	GGCGGGCCCT	TCCCCCTGGGT	GGCCGTGTGT
1740	GCCGGGGTGG	TGCTGTCCCT	CCTGCTGCTG	CTGGGCTGTG	CTGCTGTGGT	GGTCTGCGTC
1800	CGGCTGAAGC	TACAGAAACA	CCAGCCCTCCA	CCTGAACCCCT	GTGGGGGAGA	GACAGAAAACC
1860	ATGAACAACC	TAGCCAATTG	CCAGCGCGAG	AAGGACGTTT	CTGTTAGCAT	CATTGGGGCT
1920	ACCCAGATCA	AGAACACCAA	CAAGAAGGCG	GACTTTCACG	GGGACCATGG	AGCCGAGAAG
1980	AGCAGCTTTA	AGTCCGATA	CCCCACTGTG	GACTATAACC	TCGTTCCGAGA	CCTCAAGGGA
2040	GATGAAGCCA	CGTCAAGGA	TACACACAGC	AAACGTGACA	CCAAGTGCCA	GTCACAGAGC
2100	TCTGCAGGAG	AAGAGAAGAT	CGCCCCAACA	CTTAGGGGTG	GGGAGATTCC	TGACAGAAAA
2160	AGGCCAGAGT	CTGTCTACTC	TACTTCAAAG	GACACCAAGT	ACCAGTCGGT	GTATGTTCTG
2220	TCTGCAGAAA	AGGATGAGTG	TGTTATAGCG	ACTGAGGTGT	AAGATGGAAAG	CGATGTGGCA
2280	AAATTCCCAT	TTCTCTTAAA	TAAAAATTCCA	AGGATATAGC	CCCGATGAAT	GCTGCTGAGA
2340	GAGGAAGGGA	GAGGAAACCC	AGGGACTGCT	GCTGAGAAACC	AGGTTCAGGC	GAACGTGGTT
2400	CTCTCAGAGT	TAGCAGAGGC	GCCCGACACT	GCCAGCCTAG	GCTTTGGCTG	CCGCTGGACT
2460	GCCTGCTGGT	TGTTCCCATT	GCACATATGA	CAGTTGCTTT	GAAGAGTATA	TATTTAAATG
2520	GACGAGTGAC	TTGATTTCATA	TAGGAAGCAC	GCACTGCCCCA	CACGTCTATC	TTGGATTACT
2580	ATGAGCCAGT	CTTTCCTTGA	ACTAGAAAACA	CAACTGCCCTT	TATTGTCCTT	TTTGATACTG
2640	AGATGTGTTT	TTTTTTTTTC	CTAGACGGGA	AAAAGAAAAAC	GTGTGTTATT	TTTTTTTGGGA
2692	TTTGTA AAAA	TATTTTTCAT	GATTATGGGA	GAGCTCCCAA	CGCGTTGGAG	GT

FIG. 19B

MGRRSALALA	VVSALLCQVW	SSGVFELKLQ	EFVNKKGLLG	NRNCCRGSG	50
PPCACRTFFR	VCLKHYQASV	SPEPPCTYGS	AVTPVLGVDS	FSLPDCAGID	100
PAFSNPIRFP	FGFTWPGTFS	LIIEALHTDS	PDDLATENPE	RLISRLTTQR	150
HLTVGEEWSQ	DLHSSGRTDL	RYSYRFVUDE	HYGEGCSVF	CRPRDDAFGH	200
FTCGDRGEKM	CDPGWKGYC	TDPICLPGCD	DQHGVCCKPG	ECKCRVGWQG	250
RYCDECIRYP	GCLHGTCQQP	WQCNCQEGWG	GLFCNQDLNY	CTHHKPCRNG	300
ATCTNTGQGS	YTCSCRPGYT	GANCELEVDE	CAPSPCKNGA	SCTDLEDSFS	350
CTCPPPGFYGK	VCELSAMTCA	DGPCFNGGRC	SDNPDGGYTC	HCPLGFSGFN	400
CEKMDLCS	SPCSNGAKCV	DLGNSYLCRC	QAGFSGRYCE	DNVDDCASSP	450
CANGGTCRDS	VNDFSCTCP	GYTGKNCAP	VSRCEHAPCH	NGATCHQRGQ	500
RYMCECAQGY	GGPNCQFLLP	EPFPGPMVVD	LSERHMESQG	GPFPWVAVCA	550
GVVLVLLLLL	GCAAVVVCVR	LKLQKHQPPP	EPCGGETETM	NNLANCQREK	600
DVSVSIIGAT	QIKNTNKKAD	FHGDHGAES	SFKVRYPTVD	YNLVRDLKGD	650
EATVRDTHSK	RDTKCQSQSS	AGEEKIAPTL	RGGEIPDRKR	PESVYSTSKD	700
TKYQSVYVLS	AEKDECVIAT	EV			722

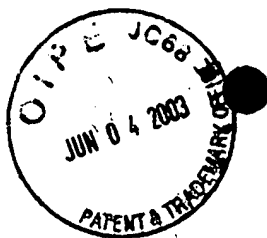
FIG. 20



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10 20 30 40 50 60
* * *
TACGATGAAY AACCTGGCGA ACTGCCAGCG TCAGAAGGAC ATCTCAGTCA GCATCATCGG

70 80 90 100 110 120
* * *
GGCYACGTCA GATCARGAAC ACCAACAAGA AGGCGGACTT YMCASCGGGG GACCASAGCG

130 140 150 160 170 180
* * *
TCCGACAAGA ATGGMTTCA AGGCCYGCTA CCCCAGCGTG GACTATAACT CGTGCAGGAC

190 200 210 220 230 240
* * *
CTCAAGGGTG ACGACACCGC CGTCAGGACG TCGCACAGCA AGCGTGACAC CAAGTGCCAG

250 260 270 280 290 300
* * *
TCCCCAGGCT CCTCAGGGAG GAGAAGGGGA CCCCAGCCAC ACTCAGGGGK TCGTGCTGC

310 320 330 340 350 360
* * *
GGGCCGGGCT CAGGAGGGGG TACCTGGGGG GTGTCTTCCT GGAACCACTG CTCCGTTTCT

FIG. 21A



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370 380 390 400 410 420
* * *
CTTCCCAAAT GTTCTCATGC ATTCATTGTG GATTTTCTCT ATTTTCCTTT TAGTGGAGAA

430 440 450 460 470 480
* * *
GCATCTGAAA GAAAAAGGCC GGA CTCGGGC TGTTC AACTT CAAAAGACAC CAAGTACCAG

490 500 510 520
* * *
TCGGTGTACG TCATATCCGA GGAGAAGGAC GAGTGCCTCA TCGCA

FIG. 21B



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* * * * *

CATTGGGTAC GGGCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCGGG

70 80 90 100 110 120

* * * * *

CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA

130 140 150 160 170 180

* * * * *

TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT

190 200 210 220 230 240

* * * * *

GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA

250 260 270 280 290 300

* * * * *

CTCCTACCGC TTCGTGTGTC ACCAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG

310 320 330 340 350 360

* * * * *

TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA

370 380 390 400 410 420

* * * * *

CCCTGGGCTCG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA

430 440 450 460 470 480

* * * * *

GCATGGATTT TGTGACAAAC CAGGGGAATG CAAGTCAGAG GTGGGCTGGC AGGGCCGGTA

490 500 510 520 530 540

* * * * *

GTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA

550 560 570 580 590 600

* * * * *

GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC

610 620 630 640 650 660

* * * * *

ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC

670 680 690 700 710 720

* * * * *

ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA

730 740 750 760 770 780

* * * * *

CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC

790 800 810 820 830 840

* * * * *

AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG

850 860 870 880 890 900

* * * * *

ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTGCGTGCT CAGACAGCCC CGATGGAGGG

FIG. 22A



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910	920	930	940	950	960
* *	* *	* *	* *	* *	* *
TACAGCTGCC	GCTGCCCCGT	GGGCTACTCC	GGCTTCAACT	GTGAGAAGAA	AATTGACTAC
970	980	990	1000	1010	1020
* *	* *	* *	* *	* *	* *
TGCAGCTCTT	CACCCTGTTC	TAATGGTGCC	AAGTGTGTGG	ACCTCGGTGA	TGCTTACCTG
1030	1040	1050	1060	1070	1080
* *	* *	* *	* *	* *	* *
TGCCGCTGCC	AGGCCGGCTT	CTCGGGGAGG	CACTGTGACG	ACAACGTGGA	CGACTGCGCC
1090	1100	1110	1120	1130	1140
* *	* *	* *	* *	* *	* *
TCCTCCCCGT	GCGCCAACGG	ACCTCGGTGA	CGGGATGGCG	TGAACGACTT	CTCCTGCACC
1150	1160	1170	1180	1190	1200
* *	* *	* *	* *	* *	* *
TGCCCCGCTG	GCTACACGGG	CAGGAACTGC	AGTGCCCCCG	CCAGCACCTG	CGAGCACGCA
1210	1220	1230	1240	1250	1260
* *	* *	* *	* *	* *	* *
CCCTGCCACA	ATGGGGCCAC	CTGCCACGAG	AGGGGCCACC	GCTATNTGTG	CGAGCACGCA
1270	1280	1290	1300	1310	1320
* *	* *	* *	* *	* *	* *
CGAAGCTACG	GGGGTCCCAA	CTCCANTTC	CTGCTCCCCC	AAACTGCCCC	CCCGGCCCCA
1330	1340	1350	1360	1370	1380
* *	* *	* *	* *	* *	* *
CGGTGGTGGA	AACTCCCCTA	AAAAAACCTA	AAAGGGCCGG	GGGGGGCCCA	TCCCCTTGGT
1390	1400	1410	1420	1430	1440
* *	* *	* *	* *	* *	* *
GGACGTGTGC	GCCGGGGTCA	TCCTTGTCTT	CATGCTGTCTG	CTGGGCTGTG	CCGCTGTGGT
1450	1460	1470	1480	1490	1500
* *	* *	* *	* *	* *	* *
GGTCTGCGTC	CGGCTGAGGC	TGCAGAAGCA	CCGGCCCCCA	GCCGACCCCT	GNCGGGGGGA
1510	1520	1530	1540	1550	1560
* *	* *	* *	* *	* *	* *
GACGGAGACC	ATGAACAACC	TGNNCAACTG	CCAGCGTGAG	AAGGACATCT	CAGTCAGCAT
1570	1580	1590	1600	1610	1620
* *	* *	* *	* *	* *	* *
CATCGGGGNC	ACGCAGATCA	AGAACACCAA	CAAGAAGGCG	GACTTCCACG	GGGACCACAG
1630	1640	1650	1660	1670	1680
* *	* *	* *	* *	* *	* *
NGCCGACAAG	AATGGCTTCA	AGGCCCGCTA	CCCAGNGGTG	GACTATAACC	TCGTGCAGGA
1690	1700	1710	1720	1730	1740
* *	* *	* *	* *	* *	* *
CCTCAAGGGT	GACGACACCG	CCGTCAGCCA	CGCGCACAGC	AAGCGTGACA	CCAAGTGNCA
1750	1760	1770	1780	1790	1800
* *	* *	* *	* *	* *	* *
GCCCCAGGGC	TCCTCAGGGG	AGGAGAAGGG	GACCCCCGAC	CCCACTCAG	GGGGTGGAGG

FIG. 22B

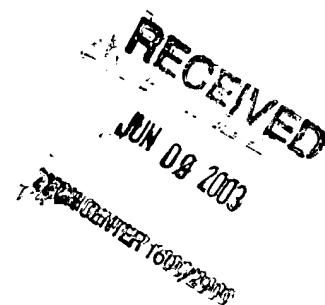


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1810	1820	1830	1840	1850	1860
* *	* *	* *	* *	* *	* *
AAGCATCTTG	AAAGAAAAAG	GCCGGACTTC	GGGCTTGTTT	AACTTTCAAA	AGACAANCAA
1870	1880	1890	1900	1910	1920
* *	* *	* *	* *	* *	* *
NGTACAAGTC	GGGTNCGTC	ATTTCCGNAG	GAGGAAGGNT	GACTGCGTCA	TAGGAANTTG
1930	1940	1950	1960	1970	1980
* *	* *	* *	* *	* *	* *
AGGTNGTAAA	NTGGNAGTTG	ANNTTGGAAG	GNNNTCCCCG	GATTCCGNTT	TCAAAGTTTT

T

FIG. 22C



GFTWPGTFSLIIEALHTDSPD>	21
<u>DLATENPERLISRLATORHL></u>	41
<u>TVGEEWSQDLHSSGRIDLKY></u>	61
<u>SYRFVCDEHYYGEGCSVFCR></u>	81
<u>PRDDAFGHFTCGERGEKVCN></u>	101
<u>PGWKGPYCTEPICLPGCDEQ></u>	121
<u>HGFCDKPGECKCRVWOGRY></u>	141
<u>CDECIRYPGCLHGTCQOPWQ></u>	161
<u>CNCOEGWGGLECNODLNYCT></u>	181
HHKPCKNGAIC* <u>TNTGQG</u> *	198
SYT* <u>PSP</u> * <u>KNGGSLTDL</u> *	213
ENSYSCTCPPGFYGKICELSAM>	235
<u>TCADGPCFNGGRCSDSPDGG></u>	255
<u>YSCRCPVGYSGFNCEKKIDY></u>	275
<u>CSSSPCSNGAKCVDLGDAYL></u>	295
<u>CRCOAGFSGRHCDDNVDDCA></u>	315
<u>SSPCANGGTCDRGVNDFSCT></u>	335
<u>CPPGYTGRNCSAPASRCEHA></u>	355
<u>PCHNGATCHERGHRY</u> *CECA>	374
<u>RSYGGPNC</u> * <u>ELLPE</u> *PPGP*>	391
<u>VV</u> * <u>LLL</u> <u>GCAAVVVCVRLRLOKH></u>	412
<u>RPPADP</u> * <u>RGETETMNNI</u> *>	428

FIG. 23A



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<u>NCOREKDISVSIIG*TOIKNTN</u>	449
<u>KKADFHGDH*ADKNGFKARYP*</u>	469
<u>VDYNLVODLKGDDTAVRDAHSKRDTK*</u>	494
<u>OPOGSSGEEKGTP*PTLR*GG*</u>	514
<u>I*RKRP*S*ST*SKD*T*</u>	526
CVI*EV*	531

FIG. 23B